

R. SWARTZ

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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/462,480
DATE: 12/29/2000
TIME: 11:58:22

Input Set : A:\ES.txt
Output Set: N:\CRF3\12292000\I462480.raw

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3 <110> APPLICANT: GICHEL, BRIGITTE
4 BERTHET, FRANCIS-XAVIER
5 ANDERSEN, PETER
6 RASMUSSEN, PETER BIRK
8 <120> TITLE OF INVENTION: POLYNUCLEOTIDE FUNCTIONALLY CODING FOR THE LHP PROTEIN FROM MYCOBACTERIUM
9 TUBERCULOSIS, ITS BIOLOGICALLY ACTIVE DERIVATIVE FRAGMENTS, AS WELL AS METHODS
10 USING THE SAME
12 <130> FILE REFERENCE: 0660-0165-0XPCT
14 <140> CURRENT APPLICATION NUMBER: 09/462,480
15 <141> CURRENT FILING DATE: 2000-03-06
17 <150> PRIOR APPLICATION NUMBER: PCT/IB98/01091
18 <151> PRIOR FILING DATE: 1998-07-16
20 <150> PRIOR APPLICATION NUMBER: 60/052,631
21 <151> PRIOR FILING DATE: 1997-07-16
23 <160> NUMBER OF SEQ ID NOS: 34
25 <170> SOFTWARE: PatentIn version 3.0
27 <210> SEQ ID NO: 1
28 <211> LENGTH: 1277
29 <212> TYPE: DNA
30 <213> ORGANISM: Mycobacterium tuberculosis
32 <400> SEQUENCE: 1
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35 gacgaggaag ccgcgcagat gggcctgctc ggcaccagtc cgtctcgaa ccatccgctg 120
37 gctgttgat caggcccccag cgcggcgccg ggcctgctgc gcgcggagtc gctacctggc 180
39 gcaggtgggt cgttgaccgc cagcgcgctg atgtctcagc tgatcgaaaa gccggttgcc 240
41 ccctcgggtg tgccggcgcc tgttgccgga tegtctgtga cgggtggcgc cgtcccggtg 300
43 ggtccgggag cgtatgggcca gggttcgcaa tccggcggtt ccaccagccc ggtctcgttc 360
45 gcgcggccac cgtctcgcca ggagcgtgaa gaagacgacg aggacyactg ggacgaagag 420
47 gacgactggt gagctcccgat aatgacaaca gacttcccggt ccacccgggc cgggaagactt 480
49 gccaacattt tggcgaggaa ygtaaaagaga gaaagtatgc cagcatggca gagatgaaga 540
51 ccgatgccgc taccctcggt caggagggcag gtaatttcga gcggatctcc ggcgacctga 600
53 aaaccagat cagccaggtg ggttcgacgg caggttcgtt gcaggggccag tggcgcgccg 660
55 cggcggggac ggcgcgccag gccgcggtg tgcgcttcca agaagcagcc aataagcaga 720
57 agcaggaact cgaagagatc tcgacgaata ttctcagggc cggcgctcaa tactcgaggg 780
59 ccgacgagga gcagcagcag gcgctgtcct cgcgaatggg cttctgacct gctaatacga 840
61 aaagaaacgg agcaaaaaa tgacagagca gcagtggat ttctcggtga tcgagccgc 900
63 ggcgaagcga atccaggga atgtcacgtc catctattcc ctcttgacg aggggaagca 960
65 gtccctgacc aagctcgcag cggcctgggg cggtagcggt tcggagggct accaggggtg 1020
67 ccagcaaaaa tgggacgcca cggctaccca gctgaacaac gcgctgcaga acctggcgcg 1080
69 gacgatcagc gaagccggtc aggcgaatggc ttgcaccgaa ggcacgctca ctgggatggt 1140
71 cgcatagggc aacgcagagt tcgcgtagaa tagcgaaca cgggatcggg cgagttcgac 1200
73 ctctcgtcgg tctcgccctt tctcgtgttt atacgttga gcyacactg agaggttgc 1260
75 atggcgcccg actacga 1277
78 <210> SEQ ID NO: 2
79 <211> LENGTH: 524
80 <212> TYPE: DNA
81 <213> ORGANISM: Mycobacterium tuberculosis

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See p. 5

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83 <400> SEQUENCE: 2
84 ctgcagcagg tgacgtcgtt gtccagccag gtgggcggca ccggcggcgg caaccagcc 60
85 gacgaggaag ccgcgcagat gggcctgtc ggcaccagtc cgtgtcgaa ccaccgctg 120
86 gctggtgat caggcccccag cggcggcggc ggcctgtcgc gcgcggagtc gctacctggc 180
87 gcagggtggg cgttgaccgc cagcgcgctg atgtctcagc tgatcgaaaa gccggttgcc 240
88 ccctcgggtg tgccggcggc tgttgccgga tcgtcgggtg cgggtggcgc cgtccgggtg 300
89 ggtccgggag cgtatgggcca ggttcgcaa tccgcggcct ccaccagccc ggtctgtg 360
90 gcgcggcgc cgtctcgcga gtagcgtgaa gaagacgac aggcagactg ggcggaagag 420
91 gacgactggt gagctccggt aatgacaaca gacttccgg ccaccgggc cggagactt 480
100 gccaacattt tggcgaggaa ggtaaagaga gaaagtatgc cagc 524
103 <210> SEQ ID NO: 3
104 <211> LENGTH: 481
105 <212> TYPE: DNA
106 <213> ORGANISM: Mycobacterium tuberculosis
108 <400> SEQUENCE: 3
109 ctgcagcagg tgacgtcgtt gtccagccag gtgggcggca ccggcggcgg caaccagcc 60
110 gacgaggaag ccgcgcagat gggcctgtc ggcaccagtc cgtgtcgaa ccaccgctg 120
111 gctggtgat caggcccccag cggcggcggc ggcctgtcgc gcgcggagtc gctacctggc 180
112 gcagggtggg cgttgaccgc cagcgcgctg atgtctcagc tgatcgaaaa gccggttgcc 240
113 ccctcgggtg tgccggcggc tgttgccgga tcgtcgggtg cgggtggcgc cgtccgggtg 300
114 ggtccgggag cgtatgggcca ggttcgcaa tccgcggcct ccaccagccc ggtctgtg 360
115 gcgcggcgc cgtctcgcga gtagcgtgaa gaagacgac aggcagactg ggcggaagag 420
116 gacgactggt gagctccggt aatgacaaca gacttccgg ccaccgggc cggagactt 480
125 g 481
128 <210> SEQ ID NO: 4
129 <211> LENGTH: 302
130 <212> TYPE: DNA
131 <213> ORGANISM: Mycobacterium tuberculosis
133 <400> SEQUENCE: 4
134 atggcagaga tgaagaccga tgcgctacc ctgcggcagg aggcaggtaa ttgcgagcg 60
135 atctccggcg acctgaaaac ccagatcgac caggtggagt cgcggcagg ttctgttcag 120
136 ggcagtggtg gcgggcgggc ggggacggcc gccaggccg cgtgtgtgcg cttccaaaga 180
137 gcagccaata agcagaagca ggaactcgac gagatctcga cgaatattcg tcaggccggc 240
138 gtccaatact cagaggccga cagggagcag cagcaggcgc tctcctcgca aatgggcttc 300
144 tg 302
147 <210> SEQ ID NO: 5
148 <211> LENGTH: 100
149 <212> TYPE: PRT
150 <213> ORGANISM: Mycobacterium tuberculosis
152 <400> SEQUENCE: 5
154 Met Ala Glu Met Lys Thr Asp Ala Ala Thr Leu Gly Gln Glu Ala Gly
155 1 5 10 15
157 Asn Phe Glu Arg Ile Ser Gly Asp Leu Lys Thr Gln Ile Asp Gln Val
158 20 25 30
160 Glu Ser Thr Ala Gly Ser Leu Gln Gly Gln Trp Arg Gly Ala Ala Gly
161 35 40 45
163 Thr Ala Ala Gln Ala Ala Val Val Arg Phe Gln Glu Ala Ala Asn Lys
164 50 55 60
166 Gln Lys Gln Glu Leu Asp Glu Ile Ser Thr Asn Ile Arg Gln Ala Gly

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167 65          70          75          80
169 Val Gln Tyr Ser Arg Ala Asp Glu Glu Gln Gln Ala Leu Ser Ser
170          85          90          95
172 Gln Met Gly Phe
173          100
175 <210> SEQ ID NO: 6
176 <211> LENGTH: 49
177 <212> TYPE: PRT
178 <213> ORGANISM: Mycobacterium tuberculosis
180 <400> SEQUENCE: 6
182 Met Ala Glu Met Lys Thr Asp Ala Ala Thr Leu Gly Gln Glu Ala Gly
183 1          5          10          15
185 Asn Phe Glu Arg Ile Ser Gly Asp Leu Lys Thr Gln Ile Asp Gln Val
186          20          25          30
188 Glu Ser Thr Ala Gly Ser Leu Gln Gly Gln Trp Arg Gly Ala Ala Gly
189          35          40          45
191 Thr
194 <210> SEQ ID NO: 7
195 <211> LENGTH: 42
196 <212> TYPE: PRT
197 <213> ORGANISM: Mycobacterium tuberculosis
199 <400> SEQUENCE: 7
201 Gln Glu Ala Ala Asn Lys Gln Lys Gln Glu Leu Asp Gly Ile Ser Thr
202 1          5          10          15
204 Asn Ile Arg Gln Ala Gly Val Gln Tyr Ser Arg Ala Asp Glu Glu Gln
205          20          25          30
207 Gln Gln Ala Leu Ser Ser Gln Met Gly Phe
208          35          40
210 <210> SEQ ID NO: 8
211 <211> LENGTH: 21
212 <212> TYPE: PRT
213 <213> ORGANISM: Mycobacterium tuberculosis
215 <400> SEQUENCE: 8
217 Gln Glu Ala Gly Asn Phe Glu Arg Ile Ser Gly Asp Leu Lys Tyr Thr
218 1          5          10          15
220 Gln Ile Asp Gln Val
221          20
223 <210> SEQ ID NO: 9
224 <211> LENGTH: 16
225 <212> TYPE: PRT
226 <213> ORGANISM: Mycobacterium tuberculosis
228 <400> SEQUENCE: 9
230 Gly Asp Leu Lys Thr Gln Ile Asp Gln Val Glu Ser Thr Ala Gly Ser
231 1          5          10          15
233 <210> SEQ ID NO: 10
234 <211> LENGTH: 16
235 <212> TYPE: PRT
236 <213> ORGANISM: Mycobacterium tuberculosis
238 <400> SEQUENCE: 10

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240 Gly Ser Leu Gln Gly Gln Trp Arg Gly Ala Ala Gly Thr Ala Ala Ala
241 1 5 10 15
243 <210> SEQ ID NO: 11
244 <211> LENGTH: 16
245 <212> TYPE: PRT
246 <213> ORGANISM: Mycobacterium tuberculosis
248 <400> SEQUENCE: 11
250 Gln Glu Ala Ala Asn Lys Gln Lys Gln Glu Leu Asp Glu Ile Ser Thr
251 1 5 10 15
253 <210> SEQ ID NO: 12
254 <211> LENGTH: 28
255 <212> TYPE: PRT
256 <213> ORGANISM: Mycobacterium tuberculosis
258 <400> SEQUENCE: 12
260 Ser Thr Asn Ile Arg Gln Ala Gly Val Gln Tyr Ser Arg Ala Asp Glu
261 1 5 10 15
263 Glu Gln Gln Gln Ala Leu Ser Ser Gln Met Gly Phe
264 20 25
266 <210> SEQ ID NO: 13
267 <211> LENGTH: 16
268 <212> TYPE: PRT
269 <213> ORGANISM: Mycobacterium tuberculosis
271 <400> SEQUENCE: 13
273 Arg Ala Asp Glu Glu Gln Gln Gln Ala Leu Ser Ser Gln Met Gly Phe
274 1 5 10 15
276 <210> SEQ ID NO: 14
277 <211> LENGTH: 21
278 <212> TYPE: DNA
279 <213> ORGANISM: Artificial/Unknown
281 <220> FEATURE:
282 <221> NAME/KEY: misc_feature
283 <222> LOCATION: ()..()
284 <223> OTHER INFORMATION: Description of Artificial Sequence: synthetic DNA
287 <400> SEQUENCE: 14
288 ctgcagcagg tgacgtcggt g 21
291 <210> SEQ ID NO: 15
292 <211> LENGTH: 23
293 <212> TYPE: DNA
294 <213> ORGANISM: Artificial/Unknown
296 <220> FEATURE:
297 <221> NAME/KEY: misc_feature
298 <222> LOCATION: ()..()
299 <223> OTHER INFORMATION: Description of Artificial Sequence: synthetic DNA
303 <400> SEQUENCE: 15
304 ccgggtggcc gggaagtctg tgt 23
307 <210> SEQ ID NO: 16
308 <211> LENGTH: 23
309 <212> TYPE: DNA
310 <213> ORGANISM: Artificial/Unknown

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```

312 <220> FEATURE:
313 <221> NAME/KEY: misc_feature
314 <222> LOCATION: ()..()
315 <223> OTHER INFORMATION: Description of Artificial Sequence: synthetic DNA
319 <400> SEQUENCE: 16
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323 <210> SEQ ID NO: 17
324 <211> LENGTH: 39
325 <212> TYPE: DNA
326 <213> ORGANISM: Artificial/Unknown
328 <220> FEATURE:
329 <221> NAME/KEY: misc_feature
330 <222> LOCATION: ()..()
331 <223> OTHER INFORMATION: Description of Artificial Sequence: synthetic DNA
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335 ggggggatcc ggtaccaggt gacgtcgttg ttcagccag 39
338 <210> SEQ ID NO: 18
339 <211> LENGTH: 39
340 <212> TYPE: DNA
341 <213> ORGANISM: Artificial/Unknown
343 <220> FEATURE:
344 <221> NAME/KEY: misc_feature
345 <222> LOCATION: ()..()
346 <223> OTHER INFORMATION: Description of Artificial Sequence: synthetic DNA
349 <400> SEQUENCE: 18
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353 <210> SEQ ID NO: 19
354 <211> LENGTH: 31
355 <212> TYPE: DNA
356 <213> ORGANISM: Artificial/Unknown
358 <220> FEATURE:
359 <221> NAME/KEY: misc_feature
360 <222> LOCATION: ()..()
361 <223> OTHER INFORMATION: Description of Artificial Sequence: synthetic DNA
364 <400> SEQUENCE: 19
365 ggggggatcc caggtgacgt cgttggttcag c 31
368 <210> SEQ ID NO: 20
369 <211> LENGTH: 31
370 <212> TYPE: DNA
371 <213> ORGANISM: Artificial/Unknown
373 <220> FEATURE:
374 <221> NAME/KEY: misc_feature
375 <222> LOCATION: ()..()
376 <223> OTHER INFORMATION: Description of Artificial Sequence: synthetic DNA
379 <400> SEQUENCE: 20
380 ggggggtacc acggtgacgt cgttggttcag c 31
383 <210> SEQ ID NO: 21
384 <211> LENGTH: 32
385 <212> TYPE: DNA

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

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L:607 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34